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The chromosome segregation in a created Musa interspecific tetraploid (AAAB) hybrid can lead to eBSV elimination

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Banana cultivars (including plantain) are derived from natural hybridization between wild diploid *Musa* species and subspecies. The main species involved are *Musa acuminata* (A genome) that is encountered in all banana cultivars, and *M. balbisiana* (B genome) in many of them.

The usual strategy to produce improved AAB plantain like hybrids exploits residual fertility of existing triploids cultivars and relies on two successive crosses. The first cross involves a plantain (AAB) and a highly fertile diploid (AA) banana to produce offsprings from which a tetraploid is selected. In a second step, this selected tetraploid is crossed with another diploid accession to produce triploid offspring from which improved hybrids may be selected. However, plantain breeding was hampered since the mid-1990s by the discovery in the B genome of infectious endogenous sequences of banana streak viruses (eBSVs), which in interspecific genome context, are able to produce BSV particles causing banana streak disease (BSD).

Understanding chromosomes segregation and recombination during meiosis, in inter-specific hybrids, is essential for breeding because it determines the possibility of combining the agronomical attributes of both species and the possibility to eliminate by crossing over undesirable traits such as eBSV. Here we monitored the distribution of infectious eBSV sequences among a F1 triploid AAB population produced by inter-specific cross between CRBP39 (AAAB) as female parent and the diploid *M. acuminata* (AA) Pahang as male. CRBP39 is a new created tetraploid carrying both infectious alleles of eBSV Goldfinger (eBSGFV) and of eBSV Obino l'ewai (eBSOLV) while Pahang do not possess any eBSV for these two BSV species. Results showed the distribution of these eBSVs was skewed toward an excess in the progeny but demonstrated that interspecific chromosome recombination occur frequently between *M. balbisiana* and *M. acuminata* genomes. Interestingly, we showed that both eBSVs were absent from 24 offsprings harboring nevertheless segment of B genome, which represent promising material for breeding. The results obtained in this study, that are based on plant material used in conventional (4x/2x) breeding strategy, open undoubtedly new positive perspectives for the safe exploitation of *M. balbisiana* characteristics in breeding programs.

Mots-clés : Banana, endogenous banana streak virus (eBSV), segregation, interspecific hybrid.